

SEQUENCE LISTING

<110> Kato, Seishi
Sekine, Shingo

<120> HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND
CDNAS ENCODING THESE PROTEINS

<130> GIN-6710CPUS

<140> 09/529,100

<141> 2000-08-21

<150> JP 0276269

<151> 1997-10-08

<150> PCT/JP98/04474

<151> 1998-10-05

<160> 28

<170> PatentIn Ver. 2.0

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<212> PRT

<213> Homo sapiens

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Glu	Ile	Ile	Lys	Arg	Ser	Glu	Phe	Val	Ile	Gly	Gln	Glu	Val	Ala	Tyr
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Gly	Glu	Gly	Val	Ser	Glu	Gln	Ala	Asn	Arg	Ala	Ile	Ser	Thr	Val	Glu
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 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
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 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
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 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
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 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110

 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
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 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
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 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
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 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
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 35 40 45
 Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala Gly
 50 55 60
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 65 70 75 80
 Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu Val
 85 90 95
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 35 40 45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
 50 55 60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
 65 70 75 80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
 85 90 95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
 100 105 110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
 115 120 125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
 130 135 140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
 145 150 155 160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
 165 170 175

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Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
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 245 250 255

Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
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Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
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Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
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Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
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 35 40 45

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Gly Met
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gatgagaccc tgtcggagag actatggggc ctgacggaga tgtttccgga gaggggtccg 180
tccgcggccg gagccacttt tgatctttcc ctctttgtgg ctacagaaaat gtacaggttt 240
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aagatc                                         426
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<213> Homo sapiens

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gatgacggat gctccccgaa caagatgaag acagtgaagt gcgcgccggg cgtggacgtc 180
tgcaccgagg ccgtgggggc ggtggagacc atccacggac aattctcgct ggcagtgcgg 240
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<222> (212)..(715)

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tgcgagaaga agaccccggc ttgagagtga g atg gcg ttt aat gat tgc ttc 232
Met Ala Phe Asn Asp Cys Phe
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agt ttg aac tac cct ggc aac ccc tgc cca ggg gac ttg atc gaa gtg 280
Ser Leu Asn Tyr Pro Gly Asn Pro Cys Pro Gly Asp Leu Ile Glu Val
10 15 20
ttc cgt cct ggc tat cag cac tgg gcc ctg tac ttg ggt gat ggt tac 328
Phe Arg Pro Gly Tyr Gln His Trp Ala Leu Tyr Leu Gly Asp Gly Tyr
25 30 35
gtt atc aac ata gca cct gta gat ggc att cct gcg tcc ttt aca agc 376
Val Ile Asn Ile Ala Pro Val Asp Gly Ile Pro Ala Ser Phe Thr Ser
40 45 50 55
gcc aag tct gta ttc agc agt aag gcc ctg gtg aaa atg cag ctc ttg 424
Ala Lys Ser Val Phe Ser Ser Lys Ala Leu Val Lys Met Gln Leu Leu
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aag gat gtt gtg gga aat gac aca tac aga ata aac aat aaa tac gat 472
Lys Asp Val Val Gly Asn Asp Thr Tyr Arg Ile Asn Asn Lys Tyr Asp
75 80 85
gaa acg tac ccc cct ctc cct gtg gaa gaa atc ata aag cgg tca gag 520
Glu Thr Tyr Pro Pro Leu Pro Val Glu Glu Ile Ile Lys Arg Ser Glu
90 95 100
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Phe Val Ile Gly Gln Glu Val Ala Tyr Asn Leu Leu Val Asn Asn Cys
105 110 115
gaa cat ttt gtg aca ttg ctt cgc tat gga gaa gga gtt tca gag cag 616
Glu His Phe Val Thr Leu Leu Arg Tyr Gly Glu Gly Val Ser Glu Gln
120 125 130 135
gcc aac cga gcg ata agt acc gtt gag ttt gtg aca gct gct gtt ggt 664
Ala Asn Arg Ala Ile Ser Thr Val Glu Phe Val Thr Ala Ala Val Gly
140 145 150
gtc ttc tca ttc ctg ggc ttg ttt cca aaa gga caa aga gca aaa tac 712
Val Phe Ser Phe Leu Gly Leu Phe Pro Lys Gly Gln Arg Ala Lys Tyr
155 160 165
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Tyr
aagaaacctg ggggtgaatac ttatttttcag tgcatcatta ctgttccaga ttcctatgat 825
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35 40 45

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50 55 60

Leu Val Lys Met Gln Leu Leu Lys Asp Val Val Gly Asn Asp Thr Tyr
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Arg Ile Asn Asn Lys Tyr Asp Glu Thr Tyr Pro Pro Leu Pro Val Glu
85 90 95

Glu Ile Ile Lys Arg Ser Glu Phe Val Ile Gly Gln Glu Val Ala Tyr

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130	135	140
Phe Val Thr Ala Ala Val Gly Val Phe Ser Phe Leu Gly Leu Phe Pro		
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<213> Homo sapiens

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<222> (25)..(516)

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Pro Gly Asp Leu Ile Glu Ile Phe Arg Leu Gly Tyr Glu His Trp Ala	
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ctg tat ata gga gat ggc tac gtg atc cat ctg gct cct cca agt gag	147
Leu Tyr Ile Gly Asp Gly Tyr Val Ile His Leu Ala Pro Pro Ser Glu	
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Tyr Pro Gly Ala Gly Ser Ser Ser Val Phe Ser Val Leu Ser Asn Ser	
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Ala Glu Val Lys Arg Glu Arg Leu Glu Asp Val Val Gly Gly Cys Cys	
60 65 70	

tat cgg gtc aac aac agc ttg gac cat gag tac caa cca cgg ccc gtg	291
Tyr Arg Val Asn Asn Ser Leu Asp His Glu Tyr Gln Pro Arg Pro Val	
75 80 85	

gag gtg atc atc agt tct gcg aag gag atg gtt ggt cag aag atg aag	339
Glu Val Ile Ile Ser Ser Ala Lys Glu Met Val Gly Gln Lys Met Lys	
90 95 100 105	

tac agt att gtg agc agg aac tgt gag cac ttt gtc acc cag ctg aga	387
Tyr Ser Ile Val Ser Arg Asn Cys Glu His Phe Val Thr Gln Leu Arg	
110 115 120	

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 Tyr Gly Lys Ser Arg Cys Lys Gln Val Glu Lys Ala Lys Val Glu Val
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 Gly Val Ala Thr Ala Leu Gly Ile Leu Val Val Ala Gly Cys Ser Phe
 140 145 150

gcg att agg aga tac caa aaa aaa gcg aca gcc tgaagcagcc acaaaatcct 536
 Ala Ile Arg Arg Tyr Gln Lys Lys Ala Thr Ala
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 35 40 45
 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
 50 55 60
 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
 65 70 75 80
 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
 85 90 95
 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
 100 105 110
 Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
 115 120 125
 Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
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Lys Ala Thr Ala

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Met Ala Pro Lys Val Phe Arg Gln Tyr Trp Asp Ile
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ccc gat ggc acc gat tgc cac cgc aaa gcc tac agc acc acc agt att 157
Pro Asp Gly Thr Asp Cys His Arg Lys Ala Tyr Ser Thr Thr Ser Ile
15 20 25

gcc agc gtc gct ggc ctg acc gcc gct gcc tac aga gtc aca ctc aat 205
Ala Ser Val Ala Gly Leu Thr Ala Ala Ala Tyr Arg Val Thr Leu Asn
30 35 40

cct ccg ggc acc ttc ctt gaa gga gtg gct aag gtt gga caa tac acg 253
Pro Pro Gly Thr Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr
45 50 55 60

ttc act gca gct gct gtc ggg gcc gtg ttt ggc ctc acc acc tgc atc 301
Phe Thr Ala Ala Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile
65 70 75

agc gcc cat gtc cgc gag aag ccc gac gac ccc ctg aac tac ttc ctc 349
Ser Ala His Val Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu
80 85 90

ggg ggc tgc gcc gga ggc ctg act ctg gga gca cgc acg cac aac tac 397
Gly Gly Cys Ala Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr
95 100 105

ggg att ggc gcc gcc gcc tgc gtg tac ttt ggc ata gcg gcc tcc ctg 445
Gly Ile Gly Ala Ala Ala Cys Val Tyr Phe Gly Ile Ala Ala Ser Leu
110 115 120

gtc aag atg ggc cgg ctg gag ggc tgg gag gtg ttt gca aaa ccc aag 493
Val Lys Met Gly Arg Leu Glu Gly Trp Glu Val Phe Ala Lys Pro Lys
125 130 135 140

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 Phe Leu Glu Gly Val Ala Lys Val Gly Gln Tyr Thr Phe Thr Ala Ala
 50 55 60
 Ala Val Gly Ala Val Phe Gly Leu Thr Thr Cys Ile Ser Ala His Val
 65 70 75 80
 Arg Glu Lys Pro Asp Asp Pro Leu Asn Tyr Phe Leu Gly Gly Cys Ala
 85 90 95
 Gly Gly Leu Thr Leu Gly Ala Arg Thr His Asn Tyr Gly Ile Gly Ala
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 Pro Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu
 20 25 30
 ctg gag gag gac gac gat gag gag cta gat gag acc ctg tcg gag aga 145
 Leu Glu Glu Asp Asp Asp Glu Glu Leu Asp Glu Thr Leu Ser Glu Arg
 35 40 45

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cta tgg ggc ctg acg gag atg ttt ccg gag agg gtc cgg tcc gcg gcc 193
Leu Trp Gly Leu Thr Glu Met Phe Pro Glu Arg Val Arg Ser Ala Ala
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gga gcc act ttt gat ctt tcc ctg ttt gtg gct cag aaa atg tac agg 241
Gly Ala Thr Phe Asp Leu Ser Leu Phe Val Ala Gln Lys Met Tyr Arg
      65                      70                      75

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Phe Ser Arg Ala Ala Leu Trp Ile Gly Thr Thr Ser Phe Met Ile Leu
      80                      85                      90                      95

gtt ctt ccc gtt gtc ttt gag acg gag aag ttg caa atg gag caa cag 337
Val Leu Pro Val Val Phe Glu Thr Glu Lys Leu Gln Met Glu Gln Gln
      100                      105                      110

cag caa ctg cag cag cgg cag ata ctt cta gga cct aac aca ggg ctg 385
Gln Gln Leu Gln Gln Arg Gln Ile Leu Leu Gly Pro Asn Thr Gly Leu
      115                      120                      125

tca gga gga atg cca ggg gct cta ccc tca ctt cct gga aag atc 430
Ser Gly Gly Met Pro Gly Ala Leu Pro Ser Leu Pro Gly Lys Ile
      130                      135                      140

tagattgtta ttgctgtttg agctgtctca gtgggataag tttgaaattc aagtgtttga 490
actgctgata atttggattt tttttttttt ttttaacttt ggcacattga tctatctaaa 550
cccgggtgggg agaattatcc ccacattgtc tcatggaaag actcaacttg caactgtgcc 610
ctccacacta tccttacttc tgtctccact ctgataccag agtgcagcca tgcagacggt 670
tattccagct ctggtcaccc gactcctttc accaaattgc tcctaactgg aagatctcac 730
tttccccttg tggggtagga accgatgcca gtgggagggg tgtgcccctg accattaacg 790
actgtttttt tttttttttt ttaaagaatg gagttgttgg ggcgggacat gcacacaatg 850
tgaaacagac aaaatgcatt acacctgtag tgtaaagtgg ccactatgaa tccctatgta 910
tgagaggagg gaggcaggct gcagcttcag ccacagaatg gggactatgg aagacagcag 970
gagctcattt cctctgcaca ttctcggtgt tagacctgtg tgtgtgttta aaaaaagaga 1030
agtcagtgtc cactttttgt atttaaatat taaaaatgat tccaactg 1078

<210> 20
<211> 142
<212> PRT
<213> Homo sapiens

<400> 20
Met Ala Ala Ala Val Ala Ala Ala Gly Ala Gly Glu Pro Gln Ser Pro
  1              5              10              15
Asp Glu Leu Leu Pro Lys Gly Asp Ala Glu Lys Pro Glu Glu Glu Leu

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20					25					30					
Glu	Glu	Asp	Asp	Asp	Glu	Glu	Leu	Asp	Glu	Thr	Leu	Ser	Glu	Arg	Leu
		35					40					45			
Trp	Gly	Leu	Thr	Glu	Met	Phe	Pro	Glu	Arg	Val	Arg	Ser	Ala	Ala	Gly
	50					55					60				
Ala	Thr	Phe	Asp	Leu	Ser	Leu	Phe	Val	Ala	Gln	Lys	Met	Tyr	Arg	Phe
65					70					75					80
Ser	Arg	Ala	Ala	Leu	Trp	Ile	Gly	Thr	Thr	Ser	Phe	Met	Ile	Leu	Val
				85				90						95	
Leu	Pro	Val	Val	Phe	Glu	Thr	Glu	Lys	Leu	Gln	Met	Glu	Gln	Gln	Gln
			100					105					110		
Gln	Leu	Gln	Gln	Arg	Gln	Ile	Leu	Leu	Gly	Pro	Asn	Thr	Gly	Leu	Ser
		115					120					125			
Gly	Gly	Met	Pro	Gly	Ala	Leu	Pro	Ser	Leu	Pro	Gly	Lys	Ile		
	130					135					140				

<210> 21
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (82)..(1119)

<400> 21
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ccaagggagc	aggacggagc	c	atg	gac	ccc	gcc	agg	aaa	gca	ggt	gcc	cag		111		
			Met	Asp	Pro	Ala	Arg	Lys	Ala	Gly	Ala	Gln				
			1				5					10				
gcc	atg	atc	tgg	act	gca	ggc	tgg	ctg	ctg	ctg	ctg	ctt	cgc	gga	159	
Ala	Met	Ile	Trp	Thr	Ala	Gly	Trp	Leu	Leu	Leu	Leu	Leu	Arg	Gly		
			15				20					25				
gga	gcg	cag	gcc	ctg	gag	tgc	tac	agc	tgc	gtg	cag	aaa	gca	gat	gac	207
Gly	Ala	Gln	Ala	Leu	Glu	Cys	Tyr	Ser	Cys	Val	Gln	Lys	Ala	Asp	Asp	
			30				35					40				
gga	tgc	tcc	ccg	aac	aag	atg	aag	aca	gtg	aag	tgc	gcg	ccg	ggc	gtg	255
Gly	Cys	Ser	Pro	Asn	Lys	Met	Lys	Thr	Val	Lys	Cys	Ala	Pro	Gly	Val	
		45				50					55					
gac	gtc	tgc	acc	gag	gcc	gtg	ggg	gcg	gtg	gag	acc	atc	cac	gga	caa	303
Asp	Val	Cys	Thr	Glu	Ala	Val	Gly	Ala	Val	Glu	Thr	Ile	His	Gly	Gln	
	60					65					70					
ttc	tcg	ctg	gca	gtg	cgg	ggt	tgc	ggt	tcg	gga	ctc	ccc	ggc	aag	aat	351

Phe	Ser	Leu	Ala	Val	Arg	Gly	Cys	Gly	Ser	Gly	Leu	Pro	Gly	Lys	Asn	
75					80					85					90	
gac	cgc	ggc	ctg	gat	ctt	cac	ggg	ctt	ctg	gcg	ttc	atc	cag	ctg	cag	399
Asp	Arg	Gly	Leu	Asp	Leu	His	Gly	Leu	Leu	Ala	Phe	Ile	Gln	Leu	Gln	
				95					100					105		
caa	tgc	gct	cag	gat	cgc	tgc	aac	gcc	aag	ctc	aac	ctc	acc	tcg	cgg	447
Gln	Cys	Ala	Gln	Asp	Arg	Cys	Asn	Ala	Lys	Leu	Asn	Leu	Thr	Ser	Arg	
			110					115					120			
gcg	ctc	gac	ccg	gca	ggg	aac	gag	agt	gca	tac	ccg	ccc	aac	ggc	gtg	495
Ala	Leu	Asp	Pro	Ala	Gly	Asn	Glu	Ser	Ala	Tyr	Pro	Pro	Asn	Gly	Val	
		125					130					135				
gag	tgc	tac	agc	tgt	gtg	ggc	ctg	agc	cgg	gag	gcg	tgc	cag	ggg	aca	543
Glu	Cys	Tyr	Ser	Cys	Val	Gly	Leu	Ser	Arg	Glu	Ala	Cys	Gln	Gly	Thr	
	140					145					150					
tcg	ccg	ccg	gtc	gtg	agc	tgc	tac	aac	gcc	agc	gat	cat	gtc	tac	aag	591
Ser	Pro	Pro	Val	Val	Ser	Cys	Tyr	Asn	Ala	Ser	Asp	His	Val	Tyr	Lys	
155					160					165					170	
ggc	tgc	ttc	gac	ggc	aac	gtc	acc	ttg	acg	gca	gct	aat	gtg	act	gtg	639
Gly	Cys	Phe	Asp	Gly	Asn	Val	Thr	Leu	Thr	Ala	Ala	Asn	Val	Thr	Val	
				175					180					185		
tcc	ttg	cct	gtc	cgg	ggc	tgt	gtc	cag	gat	gaa	ttc	tgc	act	cgg	gat	687
Ser	Leu	Pro	Val	Arg	Gly	Cys	Val	Gln	Asp	Glu	Phe	Cys	Thr	Arg	Asp	
			190					195					200			
gga	gta	aca	ggc	cca	ggg	ttc	acg	ctc	agt	ggc	tcc	tgt	tgc	cag	ggg	735
Gly	Val	Thr	Gly	Pro	Gly	Phe	Thr	Leu	Ser	Gly	Ser	Cys	Cys	Gln	Gly	
		205					210					215				
tcc	cgc	tgt	aac	tct	gac	ctc	cgc	aac	aag	acc	tac	ttc	tcc	cct	cga	783
Ser	Arg	Cys	Asn	Ser	Asp	Leu	Arg	Asn	Lys	Thr	Tyr	Phe	Ser	Pro	Arg	
	220					225					230					
atc	cca	ccc	ctt	gtc	cgg	ctg	ccc	cct	cca	gag	ccc	acg	act	gtg	gcc	831
Ile	Pro	Pro	Leu	Val	Arg	Leu	Pro	Pro	Pro	Glu	Pro	Thr	Thr	Val	Ala	
235					240					245				250		
tca	acc	aca	tct	gtc	acc	act	tct	acc	tcg	gcc	cca	gtg	aga	ccc	aca	879
Ser	Thr	Thr	Ser	Val	Thr	Thr	Ser	Thr	Ser	Ala	Pro	Val	Arg	Pro	Thr	
				255					260					265		
tcc	acc	acc	aaa	ccc	atg	cca	gcg	cca	acc	agt	cag	act	ccg	aga	cag	927
Ser	Thr	Thr	Lys	Pro	Met	Pro	Ala	Pro	Thr	Ser	Gln	Thr	Pro	Arg	Gln	
			270					275					280			
gga	gta	gaa	cac	gag	gcc	tcc	cgg	gat	gag	gag	ccc	agg	ttg	act	gga	975
Gly	Val	Glu	His	Glu	Ala	Ser	Arg	Asp	Glu	Glu	Pro	Arg	Leu	Thr	Gly	
		285					290					295				
ggc	gcc	gct	ggc	cac	cag	gac	cgc	agc	aat	tca	ggg	cag	tat	cct	gca	1023
Gly	Ala	Ala	Gly	His	Gln	Asp	Arg	Ser	Asn	Ser	Gly	Gln	Tyr	Pro	Ala	


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300          305          310
aaa ggg ggg ccc cag cag ccc cat aat aaa ggc tgt gtg gct ccc aca 1071
Lys Gly Gly Pro Gln Gln Pro His Asn Lys Gly Cys Val Ala Pro Thr
315          320          325          330

gct gga ttg gca gcc ctt ctg ttg gcc gtg gct gct ggt gtc cta ctg 1119
Ala Gly Leu Ala Ala Leu Leu Leu Ala Val Ala Ala Gly Val Leu Leu
          335          340          345

tgagcttctc cacctggaaa tttccctctc acctacttct ctggccctgg gtacccctct 1179

tctcatcact tcctgttccc accactggac tgggctggcc cagcccctgt tttccaaca 1239

ttccccagta tccccagctt ctgctgcgct gggtttgcggc tttgggaaat aaaataccgt 1299

tgtatatatt c 1310

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<210> 22
 <211> 346
 <212> PRT
 <213> Homo sapiens

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<400> 22
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr Ala
 1          5          10          15

Gly Trp Leu Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala Leu Glu
          20          25          30

Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser Pro Asn Lys
          35          40          45

Met Lys Thr Val Lys Cys Ala Pro Gly Val Asp Val Cys Thr Glu Ala
          50          55          60

Val Gly Ala Val Glu Thr Ile His Gly Gln Phe Ser Leu Ala Val Arg
          65          70          75          80

Gly Cys Gly Ser Gly Leu Pro Gly Lys Asn Asp Arg Gly Leu Asp Leu
          85          90          95

His Gly Leu Leu Ala Phe Ile Gln Leu Gln Gln Cys Ala Gln Asp Arg
          100          105          110

Cys Asn Ala Lys Leu Asn Leu Thr Ser Arg Ala Leu Asp Pro Ala Gly
          115          120          125

Asn Glu Ser Ala Tyr Pro Pro Asn Gly Val Glu Cys Tyr Ser Cys Val
          130          135          140

Gly Leu Ser Arg Glu Ala Cys Gln Gly Thr Ser Pro Pro Val Val Ser
          145          150          155          160

Cys Tyr Asn Ala Ser Asp His Val Tyr Lys Gly Cys Phe Asp Gly Asn
          165          170          175

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Val Thr Leu Thr Ala Ala Asn Val Thr Val Ser Leu Pro Val Arg Gly
 180 185 190
 Cys Val Gln Asp Glu Phe Cys Thr Arg Asp Gly Val Thr Gly Pro Gly
 195 200 205
 Phe Thr Leu Ser Gly Ser Cys Cys Gln Gly Ser Arg Cys Asn Ser Asp
 210 215 220
 Leu Arg Asn Lys Thr Tyr Phe Ser Pro Arg Ile Pro Pro Leu Val Arg
 225 230 235 240
 Leu Pro Pro Pro Glu Pro Thr Thr Val Ala Ser Thr Thr Ser Val Thr
 245 250 255
 Thr Ser Thr Ser Ala Pro Val Arg Pro Thr Ser Thr Thr Lys Pro Met
 260 265 270
 Pro Ala Pro Thr Ser Gln Thr Pro Arg Gln Gly Val Glu His Glu Ala
 275 280 285
 Ser Arg Asp Glu Glu Pro Arg Leu Thr Gly Gly Ala Ala Gly His Gln
 290 295 300
 Asp Arg Ser Asn Ser Gly Gln Tyr Pro Ala Lys Gly Gly Pro Gln Gln
 305 310 315 320
 Pro His Asn Lys Gly Cys Val Ala Pro Thr Ala Gly Leu Ala Ala Leu
 325 330 335
 Leu Leu Ala Val Ala Ala Gly Val Leu Leu
 340 345

<210> 23
 <211> 781
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (342)..(539)

<400> 23
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 aaagcggcgcg cgacggcggc gcgagaacga cccggcgggcc agttctcttc ctctgctgca 120
 cctgccctgc tcggtcagtc agtcggcggc cggcgcccgg cttgtgctca gacctcgcg 180
 ttgcggcgcc caggcccagc ggccgtagct agcgtctggc ctgagaacct cggcgctccg 240
 gcggcgcggg caccacgagc ggagcctcgc agcggctcca gaggaggcag gcgagtgagc 300
 gagtccgagg ggtggccggg gcaggtggtg gcgccgcgaa g atg gtc gcc aag caa 356
 Met Val Ala Lys Gln

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                                1                               5
agg atc cgt atg gcc aac gag aag cac agc aag aac atc acc cag cgc 404
Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys Asn Ile Thr Gln Arg
                10                        15                        20

ggc aac gtc gcc aag acc tcg aga aat gcc ccc gaa gag aag gcg tct 452
Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro Glu Glu Lys Ala Ser
                25                        30                        35

gta gga ccc tgg tta ttg gct ctc ttc att ttt gtt gtc tgt ggt tct 500
Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe Val Val Cys Gly Ser
                40                        45                        50

gca att ttc cag att att caa agt atc agg atg ggc atg tgaagtgact 549
Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met Gly Met
                55                        60                        65

gaccttaaga tgtttccatt ctctgtgaa ttttaacttg aactcattcc tgatgtttga 609

taccctgggt gaaaacaatt cagtaaagca tcctgcctca gaatgacttt cctatcatgc 669

ttcatgtgtc attccaaggt ttcttcatga gtcattccaa gttttctagt ccataccaca 729

gtgccttgca aaaaacacca catgaataaa gcaataaaat ttgattgtta ag 781

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<210> 24

<211> 66

<212> PRT

<213> Homo sapiens

<400> 24

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Met Val Ala Lys Gln Arg Ile Arg Met Ala Asn Glu Lys His Ser Lys
  1              5              10              15

Asn Ile Thr Gln Arg Gly Asn Val Ala Lys Thr Ser Arg Asn Ala Pro
      20              25              30

Glu Glu Lys Ala Ser Val Gly Pro Trp Leu Leu Ala Leu Phe Ile Phe
      35              40              45

Val Val Cys Gly Ser Ala Ile Phe Gln Ile Ile Gln Ser Ile Arg Met
      50              55              60

Gly Met
  65

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<210> 25

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: chimeric
DNA-RNA oligonucleotide

<400> 25
ggggaattcg agga

14

<210> 26
<211> 162
<212> PRT
<213> Homo sapiens

<400> 26
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
35 40 45
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
50 55 60
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65 70 75 80
Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
85 90 95
Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
100 105 110
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
115 120 125
Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
130 135 140
Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145 150 155 160
Lys Gln

<210> 27
<211> 162
<212> PRT
<213> Homo sapiens

<400> 27
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
1 5 10 15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
20 25 30

<400> 28
Met Ala Pro Lys Gln Arg Met Thr Leu Ala Asn Lys Gln Phe Ser Lys
1 5 10 15
Asn Val Asn Asn Arg Gly Asn Val Ala Lys Ser Leu Lys Pro Ala Glu
20 25 30
Asp Lys Tyr Pro Ala Ala Pro Trp Leu Ile Gly Leu Phe Val Phe Val
35 40 45
Val Cys Gly Ser Ala Val Phe Glu Ile Ile Arg Tyr Val Lys Met Gly
50 55 60